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0321

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ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,181

DATE: 03/14/2002

TIME: 12:17:40

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03142002\J086181.raw

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4 <110> APPLICANT: GIMENO, Ruth
6 <120> TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
7   DISORDERS, INCLUDING OBESITY AND DIABETES
9 <130> FILE REFERENCE: MNI-220
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/086,181
C--> 11 <141> CURRENT FILING DATE: 2002-02-26
11 <150> PRIOR APPLICATION NUMBER: 60/271,655
12 <151> PRIOR FILING DATE: 2001-02-26
14 <160> NUMBER OF SEQ ID NOS: 16
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1743
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (44)...(1129)
27 <400> SEQUENCE: 1
28 tccggactag ttctagaccg ctgcgggccc ccaggcgccg gga atg tcc cct gaa 55
29                                     Met Ser Pro Glu
30                                     1
32 tgc gcg cgg gca gcg ggc gac gcg ccc ttg cgc agc ctg gag caa gcc 103
33 Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser Leu Glu Gln Ala
34 5 10 15 20
36 aac cgc acc cgc ttt ccc ttc ttc tcc gac gtc aag ggc gac cac cgg 151
37 Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys Gly Asp His Arg
38 25 30 35
40 ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt gca 199
41 Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe Ala
42 40 45 50
44 gtg tcg ctg ctg ggc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc cga 247
45 Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg Arg
46 55 60 65
48 cga cgc cgc ggc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc gcg 295
49 Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys Ala
50 70 75 80
52 gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc tgg 343
53 Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg Trp
54 85 90 95 100
56 act gag gcc tgg ctg ctg ggc ccc gtt gcc tgc cac ctg ctc ttc tac 391
57 Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe Tyr
58 105 110 115
60 gtg atg acc ctg agc ggc agc gtc acc atc ctc acg ctg gcc gcg gtc 439

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61 Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala Val
62          120          125          130
64 agc ctg gag cgc atg gtg tgc atc gtg cac ctg cag cgc gcc gtg cgg 487
65 Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val Arg
66          135          140          145
68 ggt cct ggg cgg cgg gcg cgg gca gtg ctg ctg gcg ctc atc tgg gcc 535
69 Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp Gly
70          150          155          160
72 tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttt cga gtc gtc 583
73 Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val Val
74 165          170          175          180
76 ccg caa cgg ctc ccc gcc gcc gac cag gaa att tcg att tgc aca ctg 631
77 Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser Ile Cys Thr Leu
78          185          190          195
80 att tgg ccc acc att cct gga gag atc tcg tgg gat gtc tct ttt gtt 679
81 Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp Val Ser Phe Val
82          200          205          210
84 act ttg aac ttc ttg gtg cca gga ctg gtc att gtg atc agt tac tcc 727
85 Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val Ile Ser Tyr Ser
86          215          220          225
88 aaa att tta cag atc aca aag gca tca agg aag agg ctc acg gta agc 775
89 Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg Leu Thr Val Ser
90          230          235          240
92 ctg gcc tac tcg gag agc cac cag atc cgc gtg tcc cag cag gac ttc 823
93 Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser Gln Gln Asp Phe
94 245          250          255          260
96 cgg ctc ttc cgc acc ctc ttc ctc ctc atg gtc tcc ttc ttc atc atg 871
97 Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser Phe Phe Ile Met
98          265          270          275
100 tgg agc ccc atc atc atc acc atc ctc ctc atc ctg atc cag aac ttc 919
101 Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu Ile Gln Asn Phe
102          280          285          290
104 aag caa gac ctg gtc atc tgg ccg tcc ctc ttc ttc tgg gtg gtg gcc 967
105 Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe Trp Val Val Ala
106          295          300          305
108 ttc aca ttt gct aat tca gcc cta aac ccc atc ctc tac aac atg aca 1015
109 Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Asn Met Thr
110          310          315          320
112 ctg tgc agg aat gag tgg aag aaa att ttt tgc tgc ttc tgg ttc cca 1063
113 Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys Phe Trp Phe Pro
114 325          330          335          340
116 gaa aag gga gcc att tta aca gac aca tct gtc aaa aga aat gac ttg 1111
117 Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys Arg Asn Asp Leu
118          345          350          355
120 tcg att att tct gcc taa tttttcttta tagccgagtt totcacacct 1159
121 Ser Ile Ile Ser Gly *
122          360
124 ggcgagctgt ggcattgcttt taaacagagt tcattttccag taccctccat cagtgcaccc 1219
125 tgctttaaga aaatgaacct atgcaaatac acatccacag cgtcggtaaa ttaaggggtg 1279

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126 atcaccaagt ttcataatat tttcccttta taaaaggatt tgttgccag gtgcagtggt 1339
127 tcatgcctgt aatcccagca gtttgggagg ctgaggtggg tggatcacct gaggtcagga 1399
128 gttcgagacc aacctgacca acatggtgag acccccgtct ctactaaaaa taaaaaaaaa 1459
129 aattagctgg gagtgggtgt gggcacctgt aatcctagct acttgggagg ctgaaccagg 1519
130 agaatctctt gaacctggga ggcagagggt gcagtgaacc gagatcgtgc cattgcactc 1579
131 caaccagggc aacaagagtg aaactccatc ttaaaaaaaaa aaaaaaaaaa atttgttatg 1639
132 ggttcctttt aaatgtgaac ttttttagtg tgtttgaat atgatcaa ttaataaata 1699
133 tttatttatg actgttcagc aaaaaaaaaa aaaaaaaagg gcgg 1743
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 361
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
141 Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
142 1 5 10 15
143 Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
144 20 25 30
145 Gly Asp His Arg Leu Val Leu Ala Val Glu Thr Thr Val Leu Val
146 35 40 45
147 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
148 50 55 60
149 Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
150 65 70 75 80
151 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
152 85 90 95
153 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
154 100 105 110
155 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
156 115 120 125
157 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
158 130 135 140
159 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
160 145 150 155 160
161 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
162 165 170 175
163 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
164 180 185 190
165 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
166 195 200 205
167 Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
168 210 215 220
169 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
170 225 230 235 240
171 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
172 245 250 255
173 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
174 260 265 270
175 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
176 275 280 285

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177 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
178      290                      295                      300
179 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
180 305                      310                      315                      320
181 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
182                      325                      330                      335
183 Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
184      340                      345                      350
185 Arg Asn Asp Leu Ser Ile Ile Ser Gly
186      355                      360
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 1086
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 3
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196 aaccgcaccc gctttccctt cttctccgac gtcaaggcgc accaccggct ggtgctggcc 120
197 gcggtggaga caaccgtgct ggtgctcacc ttgacagtgt cgctgctggg caacgtgtgc 180
198 gccctggtgc tgggtggcgc cgcacgacgc cgcggcgcga ctgcctgcct ggtactcaac 240
199 ctcttctgcg cggacctgct cttcatcagc gctatccctc tgggtgctggc cgtgcgctgg 300
200 actgaggcct ggctgctggg ccccgcttgc tgccacctgc tcttctacgt gatgacctg 360
201 agcggcagcg tcaccatcct cacgctggcc gcggtcagcc tggagcgcct ggtgtgcac 420
202 gtgcacctgc agcgcggcgt gcggggctct gggcggcggg cgcgggcagt gctgctggcg 480
203 ctcatctggg gctattcggc ggtcgcctct ctgcctctct gcgtcttctt tcgagtcgtc 540
204 ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc 600
205 attcctggag agatctcgtg ggatgtctct ttgtttactt tgaacttctt ggtgccagga 660
206 ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg 720
207 ctacacgtaa gcctggccta ctcgagagc caccagatcc gcgtgtccca gcaggacttc 780
208 cggctcttcc gcacctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc 840
209 atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg 900
210 tcctcttctt tctgggtggt ggccttcaca ttgtctaatt cagccctaaa cccatcctc 960
211 tacaacatga cactgtgcag gaatgagtgg aagaaaattt ttgtgtgctt ctggttccca 1020
212 gaaaaggagg ccattttaac agacacatct gtcaaaagaa atgacttgct gattatttct 1080
213 ggctaa                                     1086
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216 <211> LENGTH: 1560
217 <212> TYPE: DNA
218 <213> ORGANISM: Murine ortholog
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (195)...(1280)
224 <400> SEQUENCE: 4
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226 ttcacaccat cagtgaccac tccagacttg tccggtttaa cccgaatctt cacagcggag 120
227 tcgatgaccc tcttgacagc cagcagcgcg cgcagctccg ccatcttccc ggacgcgtgg 180
228 gccgggcgcc cggc atg tcc cct gag tgt gca cag acg acg ggc cct ggt 230
229      Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly
230      1                      5                      10
232 ccc tcg cac acc ctg gac caa gtc aat cgc acc cac ttc cct ttc ttc 278

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233	Pro	Ser	His	Thr	Leu	Asp	Gln	Val	Asn	Arg	Thr	His	Phe	Pro	Phe	Phe	
234			15					20					25				
236	tcg	gat	gtc	aag	ggc	gac	cac	cgg	ttg	gtg	ttg	agc	gtc	gtg	gag	acc	326
237	Ser	Asp	Val	Lys	Gly	Asp	His	Arg	Leu	Val	Leu	Ser	Val	Val	Glu	Thr	
238		30					35				40						
240	acc	gtt	ctg	gga	ctc	atc	ttt	gtc	gtc	tca	ctg	ctg	ggc	aac	gtg	tgt	374
241	Thr	Val	Leu	Gly	Leu	Ile	Phe	Val	Val	Ser	Leu	Gly	Asn	Val	Cys		
242	45					50				55					60		
244	gct	cta	gtg	ctg	gtg	gcg	cgc	cgt	cgg	cgc	cgt	ggg	gcg	tca	gcc	agc	422
245	Ala	Leu	Val	Leu	Val	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Ser	Ala	Ser	
246					65				70					75			
248	ctg	gtg	ctc	aac	ctc	ttc	tgc	gcg	gat	ttg	ctc	ttc	acc	agc	gcc	atc	470
249	Leu	Val	Leu	Asn	Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Thr	Ser	Ala	Ile	
250			80					85					90				
252	cct	cta	gtg	ctc	gtc	gtg	cgc	tgg	act	gag	gcc	tgg	ctg	ttg	ggg	ccc	518
253	Pro	Leu	Val	Leu	Val	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	
254		95					100					105					
256	gtc	gtc	tgc	cac	ctg	ctc	ttc	tac	gtg	atg	aca	atg	agc	ggc	agc	gtc	566
257	Val	Val	Cys	His	Leu	Leu	Phe	Tyr	Val	Met	Thr	Met	Ser	Gly	Ser	Val	
258	110						115					120					
260	acg	atc	ctc	aca	ctg	gcc	gcg	gtc	agc	ctg	gag	cgc	atg	gtg	tgc	atc	614
261	Thr	Ile	Leu	Thr	Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	
262	125					130					135				140		
264	gtg	cgc	ctc	cgg	cgc	ggc	ttg	agc	ggc	ccg	ggg	cgg	cgg	act	cag	gcg	662
265	Val	Arg	Leu	Arg	Arg	Gly	Leu	Ser	Gly	Pro	Gly	Arg	Arg	Thr	Gln	Ala	
266					145				150					155			
268	gca	ctg	ctg	gct	ttc	ata	tgg	ggt	tac	tcg	gcg	ctc	gcc	gcg	ctg	ccc	710
269	Ala	Leu	Leu	Ala	Phe	Ile	Trp	Gly	Tyr	Ser	Ala	Leu	Ala	Ala	Leu	Pro	
270			160					165					170				
272	ctc	tac	atc	ttg	ttc	cgc	gtg	gtc	ccg	cag	cgc	ctt	ccc	ggc	ggg	gac	758
273	Leu	Tyr	Ile	Leu	Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Gly	Asp	
274		175					180					185					
276	cag	gaa	att	ccg	att	tgc	aca	ttg	gat	tgg	ccc	aac	cgc	ata	gga	gaa	806
277	Gln	Glu	Ile	Pro	Ile	Cys	Thr	Leu	Asp	Trp	Pro	Asn	Arg	Ile	Gly	Glu	
278		190					195				200						
280	atc	tca	tgg	gat	gtg	ttt	ttt	gag	act	ttg	aac	ttc	ctg	gtg	ccg	gga	854
281	Ile	Ser	Trp	Asp	Val	Phe	Phe	Glu	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	
282	205					210					215				220		
284	ctg	gtc	att	gtg	atc	agt	tac	tcc	aaa	att	tta	cag	atc	acg	aaa	gca	902
285	Leu	Val	Ile	Val	Ile	Ser	Tyr	Ser	Lys	Ile	Leu	Gln	Ile	Thr	Lys	Ala	
286			225						230				235				
288	tcg	cgg	aag	agg	ctt	acg	ctg	agc	ttg	gca	tac	tct	gag	agc	cac	cag	950
289	Ser	Arg	Lys	Arg	Leu	Thr	Leu	Ser	Leu	Ala	Tyr	Ser	Glu	Ser	His	Gln	
290			240					245					250				
292	atc	cga	gtg	tcc	caa	caa	gac	tac	cga	ctc	ttc	cgc	acg	ctc	ttc	ctg	998
293	Ile	Arg	Val	Ser	Gln	Gln	Asp	Tyr	Arg	Leu	Phe	Arg	Thr	Leu	Phe	Leu	
294			255					260					265				
296	ctc	atg	gtt	tcc	ttc	ttc	atc	atg	tgg	agt	ccc	atc	atc	atc	acc	atc	1046
297	Leu	Met	Val	Ser	Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	

VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date